UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/830,321	04/24/2001	Jennifer L. Hillman	PF-0625 USN	6725

27904 7590 11/05/2004

INCYTE CORPORATION
EXPERIMENTAL STATION
ROUTE 141 & HENRY CLAY ROAD
BLDG. E336
WILMINGTON, DE 19880

EXAMINER	
SAIDHA, TEKCHAND	
ART UNIT	**PAPER NUMBER**
1652	

DATE MAILED: 11/05/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/830,321	HILLMAN ET AL.	
	Examiner	Art Unit	
	Tekchand Saidha	1652	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *25 August 2004*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-20* is/are pending in the application.

4a) Of the above claim(s) *1,2,7,8 and 15-20* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *3-6 and 9-14* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *24 April 2001* is/are: a)☒ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

DETAILED ACTION

1. Applicants response to restriction requirement, filed August 25, 2004, is acknowledged. Applicants' proposal to re-group the claims as follows is acceptable. Accordingly, the new groups are:

Group I, claims 1-2, 15 and 19, drawn to a polypeptide (Phospholipase) of SEQ ID NO: 1 or 2, composition comprising the polypeptide and a method of treatment using the polypeptide.

Group II, claims 3-6 and 9-14, drawn to a polynucleotide of SEQ ID NO: 4 or 5, encoding the polypeptides or phospholipase of SEQ ID NO: 1 or 2.

Group III, claims 7-8, drawn to a method of detecting a polynucleotide capable of hybridization to the compliment of SEQ ID NO: 4 or 5.

Group IV claim 16, drawn to antibody to the polypeptide of SEQ ID NO: 1 or 2.

Group V claims 17-18 and 20, drawn to agonist or antagonist and method of treatment using the antagonist.

2. ***Election***

Applicant's election with traverse of Group II, filed August 25, 2004, amended claims 3-6 and 9-14, drawn to a polynucleotide of SEQ ID NO: 4 or 5, encoding the polypeptides or phospholipase of SEQ ID NO: 1 or 2, is acknowledged. The traversal is on the ground(s) that there is a **unity of invention** at least with respect to Groups I and II.

Applicants argue that as per Examiner's reasoning under PCT Rule 13.2, the polypeptide of claim 1 does not share a corresponding technical feature which is a contribution over the prior art. The Examiner noted that claim 1 recites SEQ ID NO: 1 or 2 (as amended) and fragments thereof, and therefore reads on di or tri peptide, such as the tri-peptide of Sigma (1993) item catalog no. G6887. Applicants', citing the instant specification, argue that the fragment recited in the claim is defined in the specification to be at least 5, 10, 15, 20, ...500 contiguous nucleotide or amino acids in length, and therefore does

not read upon the cited prior art, and the claimed polypeptide fragment is a contribution over the cited art and may be properly treated as a corresponding special technical feature.

Applicants arguments are well taken, however, the claims do not recite a specific size of the fragment, and is therefore, not a contribution over the cited prior art.

Although a claim should be interpreted in light of the specification disclosure, it is generally considered improper to read limitations contained in the specification into the claims. See In re Prater , 415 F.2d 1393, 162 USPQ 541 (CCPA 1969) and In re Winkhaus , 527 F.2d 637, 188 USPQ 129 (CCPA 1975), which discuss the premise that one cannot rely on the specification to impart limitations to the claim that are not recited in the claim.

Applicants' attention is further drawn to the following prior art references which teach and more than qualify to read on even the Applicants' definition of a 'fragment thereof'.

(1) USP 6,103,469 [filed 11.07.1997], showing at least 5 consecutive matches between Applicants' SEQ ID NO: 1 and USP '469 SEQ ID NO: 4 [see the enclosed sequence search alignment, REFERENCE I].

(2) USP 6,287,838 [effective filing date: 24 January, 1997], showing a homology of about 85% between Applicants' SEQ ID NO: 2 and USP '838 Accession No. AAU10696 [see the enclosed sequence search alignment, REFERENCE 2].

Beginning at the top of page 8, applicant cites Example 17, Part 2 of Annex B to the Administrative Instructions Under the PCT, which states:

Example 17

Claim 1: Protein X.

Claim 2: DNA sequence encoding protein X.

Expression of the DNA sequence in a host results in the production of a protein which is determined by the DNA sequence. The protein and the DNA sequence exhibit corresponding special technical features. Unity between claims 1 and 2 is accepted.

Applicant argues the examiner should withdraw the lack of unity requirement with respect to claims of Group I, drawn to the special technical feature of a polypeptide, and co-examine the claims of Group II with the elected claims of Group I. Applicants further argue as per PCT Rule 13.2 that Groups I and II share the same corresponding special technical feature in the protein of Group I and the DNA which encodes the protein of Group I is the DNA of Group II and, as such, should be rejoined and examined in the present application.

Applicant's argument is not found persuasive. According to PCT Rule 13.2, unity of invention exists only when the shared same or corresponding technical feature is a contribution over the prior art. The inventions of Groups I and II do not have unity of invention because the technical feature of Group I do not contribute over the prior art.

As per the rejoinder of method claims when the product claims become allowable, Applicants are referred to the previous Office Action for the rejoinder notice. Thus, the determination of lack of unity is proper under the PCT treaty.

The lack of unity determination made FINAL.

3. **Claims withdrawn**:

Claims 1-2, 7-8 & 15-20 are withdrawn from further consideration by the examiner, 37 CFR 1.142(b), as being drawn to a non-elected invention, the requirement having been traversed.

4. Claims 3-6 & 9-14 are pending and under consideration in this examination.

5. ***Priority***

Acknowledgment is made of applicants' claim for priority based on a provisional application filed 1/21/1999 and 10/27/1998.

6. ***Specification***

The specification has not been checked to the extent necessary to determine the presence of all possible minor errors. Applicant's cooperation is requested in correcting any errors of which applicant may become aware in the specification.

7. ***Continuation of prior application***

This application filed under 35 USC 119(e) lacks the necessary reference to the prior application(s). This application claims the benefit of US Provisional Application(s) No. 06/ , filed ..., should be entered following the title of the invention or as the first sentence of the specification. Also, the present status of all parent applications should be included.

8. Claims 3-6 are objected to under 37 CFR 1.75(c), as being of improper dependent form for failing to further limit the subject matter of a previous claim. Applicant is required to cancel the claim(s), or amend the claim(s) to place the claim(s) in proper dependent form, or rewrite the claim(s) in independent form. Claim 3 depends on non-elected claim 1, and placing the claim in proper dependent form will overcome this objection. Claims 4-6 are included in this objection for failing to correct the defect present in the base claim(s).

9. ***35 U.S.C. § 112, first paragraph***

Claims 3-6 & 10-14 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for a polynucleotide sequence of SEQ ID NO: 4 or 5 encoding a phospholipase of SEQ ID NO: 1 or 2, respectively, does not reasonably provide enablement for any polynucleotide sequence encoding a fragment of SEQ ID NO: 1 or 2, or which has been

modified by 10% i.e., wherein one or more amino acid residues are added, inserted or deleted or substituted and having or not having any phospholipase activity. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make the invention commensurate in scope with these claims.

The scope of the claims is not commensurate with the enablement provided by the disclosure with regard to the extremely large number of polynucleotides or fragments thereof encoding phospholipases or polypeptides broadly encompassed by the claims. Since the amino acid sequence of a protein determines its structural and functional properties, predictability of which changes can be tolerated in a protein's amino acid sequence and obtain the desired activity requires a knowledge of and guidance with regard to which amino acids in the protein's sequence, if any, are tolerant of modification and which are conserved (i.e. expectedly intolerant to modification), and detailed knowledge of the ways in which the proteins' structure relates to its function. However, in this case the disclosure is limited to the polynucleotide (SEQ ID NO: 4 or 5) and the encoded amino acid sequence(s) of Phospholipase(s) of SEQ ID NO : 1 or 2.

While recombinant and mutagenesis techniques are known, it is not routine in the art to screen for multiple substitutions or multiple modifications, as encompassed by the instant claims, and the positions within a protein's sequence where amino acid modifications can be made with a reasonable expectation of success in obtaining the desired activity/utility are limited in any protein and the result of such modifications is unpredictable. In addition, one skilled in the art would expect any tolerance to modification for a given protein to diminish with each further and additional modification, e.g. multiple substitutions.

The specification does not support the broad scope of the claims which encompass all modifications of phospholipase of SEQ ID NO: 1 or 2 by

addition, deletion, substitution or insertion, because the specification does **not** establish: (A) regions of the protein structure which may be modified without effecting phospholipase activity; (B) the general tolerance of phospholipase to modification and extent of such tolerance; (C) a rational and predictable scheme for modifying any phospholipase residues with an expectation of obtaining the desired biological function; and (D) the specification provides insufficient guidance as to which of the essentially infinite possible choices is likely to be successful.

Further no guidance is provided regarding the appropriate size of the nucleotide fragment that is capable of encoding a polypeptide fragment having the desired function. With regard to claims 5, directed to a polynucleotide sequence that hybridizes to the disclosed sequences, Applicants have not sufficiently defined the stringent conditions under which the hybridizations are to take place. Nucleic acid hybridization assays are extremely sensitive to the conditions in which they are performed. The buffer composition, pH, temperature, length of time, salt concentrations, quality and source of template nucleic acid, are all variables which determine the reproducibility of a given hybridization experiment. Given the unpredictability of the art and the nature of hybridization experiments in general, it is not sufficient to merely cite hybridization without a clear and explicit recitation of the conditions associated with the hybridization. For example, the definition of stringency as it pertains to hybridization conditions is subject to interpretation and is different from laboratory to laboratory. Therefore, without a clear and explicit recitation of the conditions which were actually used by Applicants in isolating the claimed polynucleotides which hybridize to the disclosed sequences, the skilled artisan would not be able to practice the claimed invention and would not be reasonably apprised of the metes and bounds of the claimed invention. Without such guidance, the experimentation left to those skilled in the art is undue. Including in the claims the exact nature of the hybridization conditions

used to isolate the claimed polynucleotides would aid in overcoming this portion of the rejection.

Thus, applicants have not provided sufficient guidance to enable one of ordinary skill in the art to make and use the claimed invention in a manner reasonably correlated with the scope of the claim broadly including obtaining polynucleotide encoding phospholipase(s) by enormous number of amino acid modifications of SEQ ID NO: 1 or 2 or fragments thereof. The scope of the claims must bear a reasonable correlation with the scope of enablement (In re Fisher, 166 USPQ 19 24 (CCPA 1970)). Without sufficient guidance, determination of such polynucleotides encoding polypeptides having the desired enzymatic characteristics is unpredictable and the experimentation left to those skilled in the art is improper and undue in making a polynucleotide or fragment thereof capable of encoding the claimed modified or variant polypeptide. See In re Wands 858 F.2d 731, 8 USPQ2nd 1400 (Fed. Cir, 1988).

10. ***35 U.S.C. § 112, first paragraph (Written Description)***

Claims 3-6 & 10-14 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventors, at the time the application was filed, had possession of the claimed invention.

Claims 3-6 & 10-14 recite species of polynucleotides which are fragments/or are variants and having 90% sequence identity to polynucleotide sequences of SEQ ID NO: 4 or 5 or polynucleotide variant encoding polypeptide sequence(s) of SEQ ID NO: 1 or 2, or fragments thereof.

The specification, however, only provides 2 representative species of polynucleotide (or DNA) from *Homo sapiens* of SEQ ID Nos: 4 and 5, encoding the protein of SEQ ID Nos. 1 and 2 (phospholipases). There is no disclosure of any particular structure to function/activity relationship in the single disclosed species to other species where such sequences are conserved in order to

establish a relationship among species or modify the DNA/enzyme by substitution or make a polynucleotide at least 90% identical to SEQ ID NO : 4 or 5 and encode a protein having phospholipase activity. The specification also fails to describe additional representative species of these phospholipases by any identifying structural characteristics other than the properties or activity recited in claims, for which no predictability of structure is apparent. Given this lack of additional representative species, such as the modifications of at least 10% of the amino acid residues of SEQ ID NO : 1 or 2 by modifying the DNA of SEQ ID NO: 4 or 5, and still retain phospholipase activity, or provide a DNA that will hybridize under stringent conditions and still encode a protein with Phospholipase activity, or provide DNA fragment(s) of specific size(s) encoding active protein fragments, Applicants have failed to sufficiently describe the claimed invention, in such full, clear, concise, and exact terms that a skilled artisan would recognize Applicants were in possession of the claimed invention.

Therefore, the written description requirement is not satisfied.

11. ***Claim Rejections - 35 USC § 112*** (second paragraph)

Claims 9-11 are rejected under 35 U.S.C.§ 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claim 9, line 1, recites 'polynucleotide comprising a polypeptide'. The claim is indefinite because a polynucleotide cannot comprise a polypeptide. A polynucleotide can encode a polypeptide or a polynucleotide can comprise of nucleotides. Further, the sequences of SEQ ID Nos. 4 and 5 are polynucleotide sequences, not polypeptides sequences, as recited in the claim. Amending the claim to recite ".....polynucleotide encoding a polypeptide sequence selected from the group consisting of SEQ OD NO: 1 and 2", is suggested to overcome this rejection.

Claims 10-11 are included in the rejection for failing to correct the defect present in the base claim(s).

12. ***Claim Rejections - 35 USC § 102***

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.
> (e) the invention was described in a patent granted on an application for patent by another filed in the United States before the invention thereof by the applicant for patent, or on an international application by another who has fulfilled the requirements of paragraphs (1), (2), and (4) of section 371(c) of this title before the invention thereof by the applicant for patent.

Claims 3-6 & 12-14 are rejected under 35 U.S.C. 102(e) as being anticipated by Hawkins et al. [USP 6,103,469, **REFERENCE I,** 11/7/1997]. Hawkins et al. teach nucleic acid that encode fragment of SEQ ID NO: 1 [See the enclosed sequence search alignment between Applicants SEQ ID NO: 1 and USP 6,103,469 SEQ ID NO: 4]. Vectors, host cells and method of making the polypeptide is described in the patent [see claims and the entire patent]. The reference reads on the claim limitations: (1) a polynucleotide encoding a polypeptide fragment of SEQ ID NO: 1 or 2, wherein the polypeptide size remains undefined; (2) a polynucleotide variant having at least 90% polynucleotide sequence identity to the polynucleotide of claim 3 [claim 3 depends on claim 1] which is drawn to a polypeptide fragment of SEQ ID NO: 1 or 2, wherein the polypeptide size remains undefined, which translates to 90% identity to the polynucleotide fragment of undefined size; and such a sequence fragment (3) will hybridize to the fragment of the reference and (4) for which the complementary sequence can be deduced by the base pairing rule, where in a

double-helical nucleic acid structure adenine must form a base pair with thymine (or uracil) and cytosine must form a base pair with guanine, and vice verse. The reference anticipates the claims.

13. Claims 3-6 & 12-14 are rejected under 35 U.S.C. 102(e) as being anticipated by Kriz et al. [USP 6287838, **REFERENCE II**, 1/24/1997]. Kriz et al. teach nucleic acid that encodes a phospholipase, wherein the amino acid sequence of the Phospholipase [Accession No. AAU10696] is 85.5% identical to Applicants SEQ ID NO: 2 [See the enclosed sequence search alignment between Applicants SEQ ID NO: 2 and Accession No. AAU10696]. Vectors, host cells and method of making the polypeptide is described in the patent [see claims and the entire patent].

14. Claims 3-6 & 12-14 are rejected under 35 U.S.C. 102(e) as being anticipated by Sharp et al. [USP 6025178, **REFERENCE III**, 03/28/1997]. Sharp et al. teach nucleic acid that encodes a phospholipase, wherein the amino acid sequence of the Phospholipase [Accession No. AAY51557] is 85.5% identical to Applicants SEQ ID NO: 2 [See the enclosed sequence search alignment between Applicants SEQ ID NO: 2 and Accession No. AAY51557]. Vectors, host cells and method of making the polypeptide is described in the patent [see claims and the entire patent].

15. Claims 3-6 are rejected under 35 U.S.C. 102(b) as being anticipated by Vial et al. [J. Biol. Chem. 270(29), 17327-32, 1995, **REFERENCE IV**]. Vial et al. teach nucleic acid that encode fragment of SEQ ID NO: 4 [See the enclosed sequence search alignment between Applicants SEQ ID NO: 4 and Accession No. X82631]. 11-12 contiguous nucleotide matches between the two sequences are circled in the alignment appended to the JBC reference. The reference reads on the claim limitations: (1) a polynucleotide encoding a polypeptide fragment of SEQ ID NO: 1 or 2, wherein the polypeptide size remains undefined; (2) a polynucleotide variant having at least 90% polynucleotide sequence identity to the polynucleotide of claim 3 [claim 3 depends on claim 1]

which is drawn to a polypeptide fragment of SEQ ID NO: 1 or 2, wherein the polypeptide size remains undefined, which translates to 90% identity to the polynucleotide fragment of undefined size; and such a sequence fragment (3) will hybridize to the fragment of the reference and (4) for which the complementary sequence can be deduced by the base pairing rule, where in a double-helical nucleic acid structure adenine must form a base pair with thymine (or uracil) and cytosine must form a base pair with guanine, and vice verse. The reference anticipates the claims.

16. Claims 3-6 are rejected under 35 U.S.C. 102(a) as being anticipated by Accession No. AA762051 [**REFERENCE V**, 1/27/1998]. Accession No. AA762051 is 45.4% identical to Applicants' DNA sequence of SEQ ID NO: 4. The reasons are as explained in paragraph 15, above.

17. Claims 3-6 & 12-14 are rejected under 35 U.S.C. 102(e) as being anticipated by Kriz et al. [USP 6287838, **REFERENCE VI**, 1/24/1997] or Choiu et al. [USP 6242206, **REFERENCE VII**, 3/28/1997]. Kriz et al. or Choiu et al. teach nucleic acid that encodes a phospholipase, wherein the nucleic acid sequence [Accession No. AR168355] is 82% [or 82.4%, as per Choiu et al.] identical to Applicants SEQ ID NO: 5 [See the enclosed sequence search alignment between Applicants SEQ ID NO: 5 and Accession No. AR168355 or AR156370]. Vectors, host cells and method of making the polypeptide is described in the patent [see claims and the entire patent]. Further reasoning is as outlined in paragraph 15, above.

18. No claim is allowed.

19. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Tekchand Saidha (Ph.D.) whose telephone number is (571) 272-0940. The examiner can normally be reached on Monday-Friday from 8:15 am to 4:45 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ponnathapu Achutamurthy, can be reached at (571)

272-0928. The fax phone number for this Group in the Technology Center is 703 872-9306.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the Group receptionist whose telephone number is 571 272-1600.

Tekchand Saidha
Primary Examiner, Art Unit 1652
Recombinant Enzymes, E03A61 Remsen Bld.
400 Dulany Street, Alexandria, VA
Telephone : (571) 272-0940

November 3, 2004

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 5, 2004, 19:10:14 ; Search time 9.08667 Seconds
(without alignments)
823.819 Million cell updates/sec

Title: US-09-830-321A-1
Perfect score: 852
Sequence: 1 MELALLCGLVVMAGVIPIQG.....YQKRLRFYWRPHCRGQTPGC 145

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	401.5	47.1	146	3	US-08-966-317-4	Sequence 4, Appli
2	401.5	47.1	146	4	US-09-489-770-4	Sequence 4, Appli
3	400.5	47.0	146	2	US-08-888-497-35	Sequence 35, Appl
4	400.5	47.0	146	4	US-09-362-230-35	Sequence 35, Appl
5	400.5	47.0	146	5	PCT-US94-07926-35	Sequence 35, Appl
6	395.5	46.4	144	1	US-08-186-895-10	Sequence 10, Appl
7	395.5	46.4	144	2	US-08-888-497-37	Sequence 37, Appl
8	395.5	46.4	144	4	US-09-362-230-37	Sequence 37, Appl
9	395.5	46.4	144	5	PCT-US94-07926-37	Sequence 37, Appl
10	371.5	43.6	146	3	US-08-966-317-3	Sequence 3, Appli
11	371.5	43.6	146	4	US-09-489-770-3	Sequence 3, Appli
12	367.5	43.1	124	1	US-08-170-360-4	Sequence 4, Appli
13	367.5	43.1	124	2	US-08-888-497-39	Sequence 39, Appl
14	367.5	43.1	124	4	US-09-362-230-39	Sequence 39, Appl
15	367.5	43.1	124	4	US-09-740-569-2	Sequence 2, Appli
16	367.5	43.1	124	5	PCT-US94-07926-39	Sequence 39, Appl
17	360	42.3	125	2	US-08-888-497-42	Sequence 42, Appl
18	360	42.3	125	4	US-09-362-230-42	Sequence 42, Appl
19	360	42.3	125	5	PCT-US94-07926-42	Sequence 42, Appl
20	347	40.7	138	2	US-08-888-497-32	Sequence 32, Appl
21	347	40.7	138	4	US-09-362-230-32	Sequence 32, Appl
22	347	40.7	138	5	PCT-US94-07926-32	Sequence 32, Appl
23	332	39.0	125	1	US-08-170-360-5	Sequence 5, Appli
24	329.5	38.7	122	1	US-07-734-534A-1	Sequence 1, Appli
25	328.5	38.6	118	2	US-08-888-497-40	Sequence 40, Appl
26	328.5	38.6	118	4	US-09-097-094-5	Sequence 5, Appli
27	328.5	38.6	118	4	US-09-362-230-40	Sequence 40, Appl
28	328.5	38.6	118	5	PCT-US94-07926-40	Sequence 40, Appl
29	315.5	37.0	137	2	US-08-888-497-30	Sequence 30, Appl
30	315.5	37.0	137	4	US-09-362-230-30	Sequence 30, Appl
31	315.5	37.0	137	5	PCT-US94-07926-30	Sequence 30, Appl
32	305.5	35.9	117	2	US-08-888-497-44	Sequence 44, Appl
33	305.5	35.9	117	4	US-09-362-230-44	Sequence 44, Appl
34	305.5	35.9	117	5	PCT-US94-07926-44	Sequence 44, Appl
35	295.5	34.7	130	2	US-08-888-497-43	Sequence 43, Appl
36	295.5	34.7	130	4	US-09-362-230-43	Sequence 43, Appl
37	295.5	34.7	130	5	PCT-US94-07926-43	Sequence 43, Appl
38	295.5	34.7	158	2	US-08-888-497-22	Sequence 22, Appl
39	295.5	34.7	158	4	US-09-362-230-22	Sequence 22, Appl
40	295.5	34.7	158	5	PCT-US94-07926-22	Sequence 22, Appl
41	263.5	30.9	165	3	US-08-966-317-1	Sequence 1, Appli
42	263.5	30.9	165	4	US-09-489-770-1	Sequence 1, Appli
43	242.5	28.5	148	2	US-08-888-497-36	Sequence 36, Appl
44	242.5	28.5	148	4	US-09-362-230-36	Sequence 36, Appl
45	242.5	28.5	148	5	PCT-US94-07926-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-08-966-317-4
; Sequence 4, Application US/08966317
; Patent No. 6103469
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Bandman, Olga
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/966,317
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0403 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 204319
US-08-966-317-4

Query Match 47.1%; Score 401.5; DB 3; Length 146;
Best Local Similarity 47.9%; Pred. No. 1.1e-34;

REFERENCE 1

11/7/1997 (filing)

Matches 70; Conservative 23; Mismatches 52; Indels 1; Gaps 1;

```
Qy          1 MELALLCGLVVMA-GVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDA 59
              |:: ||  :|:|| | | :|| :|   :|:   |||   :||  ||||||:||||||||
Db          1 MKVLLLLAVVIMAFGSIQVQGSLLEFGQMILFKTGKRADVSYGFYGCHCGVGGRGSPKDA 60

Qy         60 TDWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCL 119
              ||||| ||||||: |: :|||     |:::: | | ||     | :||| ||| | ||
Db         61 TDWCCVTHDCCYNRLEKRGCGTKFLTYKFSYRGGQISCSTNQDSCRKQLCQCDKAAAECF 120

Qy        120 KRNLDTYQKRLRFYWRPHCRGQTPGC 145
              ||  :|  : :||    |:|:|| |
Db        121 ARNKKSYSLKYQFYLNKFCKGKTPSC 146
```

RESULT 2
US-09-489-770-4
; Sequence 4, Application US/09489770
; Patent No. 6399301
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Bandman, Olga
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/489,770
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/966,317
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0403 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 204319
US-09-489-770-4

Query Match 47.1%; Score 401.5; DB 4; Length 146;
Best Local Similarity 47.9%; Pred. No. 2.1e-34;
Matches 70; Conservative 23; Mismatches 52; Indels 1; Gaps 1;

```
Qy          1 MELALLCGLVVMA-GVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDA 59
              |:: ||  :|:|| | | :|| :|   :|:   |||   :||  ||||||:||||||||
Db          1 MKVLLLLAVVIMAFGSIQVQGSLLEFGQMILFKTGKRADVSYGFYGCHCGVGGRGSPKDA 60

Qy         60 TDWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCL 119
              ||||| ||||||: |: :|||     |:::: | | ||     | :||| ||| | ||
Db         61 TDWCCVTHDCCYNRLEKRGCGTKFLTYKFSYRGGQISCSTNQDSCRKQLCQCDKAAAECF 120

Qy        120 KRNLDTYQKRLRFYWRPHCRGQTPGC 145
              ||  :|  : :||    |:|:|| |
Db        121 ARNKKSYSLKYQFYLNKFCKGKTPSC 146
```

RESULT 3
US-08-888-497-35
; Sequence 35, Application US/08888497
; Patent No. 5972677
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,497
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/651,405
; FILING DATE:
; APPLICATION NUMBER: US 08/097,354
; FILING DATE: 26-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-888-497-35

Query Match 47.0%; Score 400.5; DB 2; Length 146;
Best Local Similarity 47.9%; Pred. No. 1.4e-34;
Matches 70; Conservative 23; Mismatches 52; Indels 1; Gaps 1;

```
Qy          1 MELALLCGLVVMA-GVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDA 59
              |:: ||  :|:|| | | :|| :|   :|:   |||   :||  ||||||:||||||||
Db          1 MKVLLLLAVVIMAFGSIQVQGSLLEFGQMILFKTGKRADVSYGFYGCHCGVGGRGSPKDA 60

Qy         60 TDWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCL 119
              ||||| ||||||: |: :|||     |:::: | | ||     | :||| ||| | ||
Db         61 TDWCCVTHDCCYNRLEKRGCGTKFVTYKFSYRGGQISCSTNQDSCRKQLCQCDKAAAECF 120

Qy        120 KRNLDTYQKRLRFYWRPHCRGQTPGC 145
              ||  :|  : :||    |:|:|| |
Db        121 ARNKKSYSLKYQFYPNKFCKGKTPSC 146
```

```
FT   Modified-site   566
FT                   /label= potential_phosphorylation_site
XX
PN   WO200024911-A2.
XX
PD   04-MAY-2000.
XX
PF   27-OCT-1999;   99WO-US025021.
XX
PR   27-OCT-1998;   98US-00181317.
PR   21-JAN-1999;   99US-00234726.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Hillman JL,  Bandman O,  Guegler KJ,  Corley NC,  Baughn MR;
PI   Azimzai Y,  Lal P,  Lu DAM;
XX
DR   WPI; 2000-350750/30.
DR   N-PSDB; AAA53270.
XX
PT   Human phospholipase genes and proteins useful to diagnose, prevent or
PT   treat cancer, autoimmune or inflammatory or reproductive disorders.
XX
PS   Disclosure; Page 71-72; 80pp; English.
XX
CC   The present sequence is human phospholipase 2 (HPPL2). This protein is
CC   involved in the hydrolysis of membrane phospholipids. The protein and its
CC   coding sequence can be used to diagnose and treat the following: cancers
CC   such as prostate, breast and testicular cancers, autoimmune and
CC   inflammatory disorders such as AIDS, allergies, anaemia, asthma,
CC   atherosclerosis, Crohn's disease, diabetes mellitus, emphysema, Graves'
CC   disease, irritable bowel syndrome, multiple sclerosis, myasthenia gravis,
CC   psoriasis, rheumatoid arthritis and systemic lupus erythematosus,
CC   infection caused by viruses, fungi, bacteria, parasites and protozoa, and
CC   reproductive disorders including infertility, disruptions of the
CC   menstrual cycle, polycystic ovary syndrome, ectopic pregnancies,
CC   disruptions of spermatogenesis, cancers within the reproductive tract and
CC   impotence
XX
SQ   Sequence 605 AA;

  Query Match             100.0%;  Score 3235;  DB 3;  Length 605;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-292;
  Matches  605;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MIFVELSPTLALCLERVASHLTDTGLLVLFCPAPCPFFFFFEMESLSVAQAGVQWRDLGS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MIFVELSPTLALCLERVASHLTDTGLLVLFCPAPCPFFFFFEMESLSVAQAGVQWRDLGS 60

Qy         61 LQPPPLGFKRFSCLSLPSSWDYRLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LQPPPLGFKRFSCLSLPSSWDYRLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQL 120

Qy        121 DGDLQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DGDLQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLY 180

Qy        181 EDPEWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 EDPEWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALI 240

Qy        241 NEALLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQGLTTFEFGEWCEFSPYEVGFP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NEALLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFP 300

Qy        301 KYGAFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDR 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KYGAFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDR 360

Qy        361 WVRNQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 WVRNQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQ 420
```

```
Qy        421 HPHFSTWKATTLI                LDVGYLINTSCLPLLQPTRDVDLILSLDYNLH 480
              |||||||||||||                |||||||||||||||||||||||||||||||||
Db        421 HPHFSTWKATTLI                LDVGYLINTSCLPLLQPTRDVDLILSLDYNLH 480

Qy        481 GAFQQLQLLGRF                  EQLQPRECHTFSDPTCPGAPAVLHFSSGVRRT 540
              ||||||||||||                  ||||||||||||||||||||||||||||||||
Db        481 GAFQQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHFSSGVRRT 540

Qy        541 PEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRRR 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 PEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRRR 600

Qy        601 QRRPH 605
              |||||
Db        601 QRRPH 605
```

RESULT 2
AAU10696
ID   AAU10696 standard; protein; 778 AA.
XX
AC   AAU10696;
XX
DT   25-FEB-2002 (first entry)
XX
DE   Human cPLA2-beta enzyme.
XX
KW   Calcium-independent cytosolic phospholipase A2-beta; cPLA2-beta;
KW   U937 cell; membrane phospholipid turnover; intracellular signalling;
KW   arachidonic acid cascade; inflammatory disorder; rheumatoid arthritis;
KW   psoriasis; asthma; inflammatory bowel disease; antiinflammatory.
XX
OS   Homo sapiens.
XX
PN   US6287838-B1.
XX
PD   11-SEP-2001.
XX
PF   13-DEC-1999;   99US-00460145.
XX
PR   24-JAN-1997;   97US-00788975.
XX
PA   (GEMY) GENETICS INST INC.
XX
PI   Kriz R, Song C;
XX
DR   WPI; 2002-054342/07.
DR   N-PSDB; AAS17362.
XX
PT   Novel cytosolic phospholipase A2-beta enzyme encoding polynucleotide,
PT   useful for producing the enzyme for use in assays to discover enzyme
PT   antagonists.
XX
PS   Claim 1; Col 15-19; 19pp; English.
XX
CC   The present invention relates to a novel calcium-independent cytosolic
CC   phospholipase A2 (cPLA2)-beta enzyme and the cDNA sequence encoding it.
CC   The cDNA clone is isolated from U937 cells. The cPLA2 enzyme is active in
CC   membrane phospholipid turnover and in regulation of intracellular
CC   signalling mediated by the arachidonic acid cascade. The invention
CC   describes a method for producing phospholipase enzymes which can be used
CC   to identify inhibitors of their function. The inhibitors can used to
CC   treat inflammatory disorders such as rheumatoid arthritis, psoriasis,
CC   asthma, and inflammatory bowel disease. The present sequence represents
CC   human cPLA2-beta enzyme
XX
SQ   Sequence 778 AA;

  Query Match   85.5%; Score 2767.5; DB 5; Length 778;
  Best Local Similarity   87.6%; Pred. No. 2.5e-248;
  Matches 537; Conservative   5; Mismatches   22; Indels   49; Gaps   6;

Qy   24 TGLLVLFCPAPCPFFFFFEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYR 83
```
```

```
Db        184 TGTFRFHCPA-C-----WEQE-LSI-----------RLQDAPEEQLKAPLSALPSGQVVR 225

Qy         84 --------------------LRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 123

Db        226 LVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 285

Qy        124 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 183

Db        286 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 345

Qy        184 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA 243

Db        346 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA 405

Qy        244 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 303

Db        406 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 465

Qy        304 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 363

Db        466 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 525

Qy        364 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 423

Db        526 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 585

Qy        424 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 483

Db        586 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 645

Qy        484 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF---------- 533

Db        646 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHFPLVSDSFREY 705

Qy        534 -SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 592

Db        706 SAPGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 765

Qy        593 RQAVQRRRQRRPH 605

Db        766 RQAVQRRRQRRPH 778
```

RESULT 3
ABG76482
ID ABG76482 standard; protein; 778 AA.
XX
AC ABG76482;
XX
DT 10-MAY-2003 (first entry)
XX
DE Human partial cytosolic phospholipase A2-beta, cPLA2-beta.
XX
KW Human; calcium independent cytosolic phospholipase A2-beta; cPLA2-beta;
KW antiinflammatory; arachidonic acid cascade; enzyme;
KW inflammatory condition.
XX
OS Homo sapiens.
XX
PN US6482625-B1.
XX
PD 19-NOV-2002.
XX
PF 29-JUN-2001; 2001US-00895547.
XX
PR 24-JAN-1997; 97US-00788975.
PR 13-DEC-1999; 99US-00460145.
XX
PA (GEMY) GENETICS INST LLC.
XX
PI Kriz R, Song C;
XX
DR WPI; 2003-287361/28.
DR N-PSDB; ABX11883.
XX
PT Novel purified calcium-independent cytosolic phospholipase A2-beta
PT enzyme, useful for screening compounds having antiinflammatory activity
PT mediated by the arachidonic acid cascade.
XX
PS Claim 2; Col 13-18; 19pp; English.
XX
CC The invention relates to a purified phospholipase enzyme (calcium-
CC independent cytosolic phospholipase A_2-beta enzyme) peptide appearing as
CC ABG76482 encoded by a polynucleotide appearing as ABX118883. The protein
CC has an enzymatic activity in a mixed micelle assay (MMA) with 1-palmitoyl
CC -2- (1^4C)-arachidonyl- phosphatidylcholine. cPLA2-beta is useful for
CC assaying chemical agents for antiinflammatory activity mediated by the
CC various components of the arachidonic acid cascade. cPLA2-beta is also
CC useful in the development of polyclonal and monoclonal antibodies which
CC are useful as research or diagnostic tools, and to study phospholipase
CC A_2 activity and inflammatory conditions. The present sequence represents
CC a partial cPLA2-beta protein
XX
SQ Sequence 778 AA;

Query Match 85.5%; Score 2767.5; DB 6; Length 778;
Best Local Similarity 87.6%; Pred. No. 2.5e-248;
Matches 537; Conservative 5; Mismatches 22; Indels 49; Gaps 6;

```
Qy         24 TGLLVLFCPAPCFFFFFEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYR 83

Db        184 TGTFRFHCPA-C-----WEQE-LSI-----------RLQDAPEEQLKAPLSALPSGQVVR 225

Qy         84 --------------------LRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 123

Db        226 LVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 285

Qy        124 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 183

Db        286 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 345

Qy        184 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA 243

Db        346 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA 405

Qy        244 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 303

Db        406 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 465

Qy        304 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 363

Db        466 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 525

Qy        364 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 423

Db        526 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 585

Qy        424 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 483

Db        586 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 645

Qy        484 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF---------- 533

Db        646 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHFPLVSDSFREY 705

Qy        534 -SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 592

Db        706 SAPGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 765

Qy        593 RQAVQRRRQRRPH 605

Db        766 RQAVQRRRQRRPH 778
```

RESULT 4

```
CC   are useful as research or diagnostic tools, and to study phospholipase
CC   A_2 activity and inflammatory conditions. The present sequence represents
CC   the cPLA2-beta protein
XX
SQ   Sequence 797 AA;

  Query Match           85.5%;  Score 2767.5;  DB 6;  Length 797;
  Best Local Similarity  87.6%;  Pred. No. 2.6e-248;
  Matches  537;  Conservative    5;  Mismatches   22;  Indels   49;  Gaps    6;

Qy         24 TGLLVLFCPAPCPFFFFEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYR 83
              ||    ||| |     :| | ||:           ||  |    :    :|||   |
Db        203 TGTFRFHCPA-C-----WEQE-LSI----------RLQDAPEEQLKAPLSALPSGQVVR 244

Qy         84 --------------------LRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 123
                                  ||||||||||||||||||||||||||||||||||||||||
Db        245 LVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 304

Qy        124 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 364

Qy        184 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        365 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA 424

Qy        244 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        425 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 484

Qy        304 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        485 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 544

Qy        364 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        545 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 604

Qy        424 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        605 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 664

Qy        484 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF---------- 533
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        665 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHFPLVSDSFREY 724

Qy        534 -SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 592
               : ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        725 SAPGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 784

Qy        593 RQAVQRRRQRRPH 605
              |||||||||||||
Db        785 RQAVQRRRQRRPH 797


RESULT 6
AAY51557
ID   AAY51557 standard; protein; 913 AA.
XX
AC   AAY51557;
XX
DT   18-MAY-2000  (first entry)
XX
DE   Human PLA2 protein.
XX
KW   PLA2; phospholipase A2; phosphatide 2-acyl hydrolase; human; therapy;
KW   arachidonic acid; lysophospholipid; Alzheimer's disease.
XX
OS   Homo sapiens.
XX
PN   US6025178-A.
XX
PD   15-FEB-2000.
XX
PF   28-MAR-1997;   97US-00827208.
XX
PR   29-MAR-1996;   96US-0014608P.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Sharp JD,  Strifler BA,  Choiu XC,  Kramer RM,  Pickard RT;
XX
DR   WPI; 2000-181816/16.
DR   N-PSDB; AAZ88756, AAZ88757.
XX
PT   An isolated amino acid having phospholipase (PL)A2 activity is useful in
PT   assays to identify inhibitors having a therapeutic benefit, such as
PT   inhibiting the central role of PLA2 in the inflammatory component of
PT   Alzheimer's disease.
XX
PS   Claim 1; Col 53-58; 32pp; English.
XX
CC   This invention describes a novel human phospholipase A2 (PLA2) protein
CC   (I) and its encoding nucleic acid. The amino acid (I) releases
CC   arachidonic acid in specific tissues characterized by unique membrane
CC   phospholipids, by generating lysophospholipid species which are
CC   deleterious to membrane integrity or by remodeling of unsaturated species
CC   of membrane phospholipids through deacylation/reacylation mechanisms. The
CC   amino acid is useful in assays to identify inhibitors having a
CC   therapeutic benefit, such as inhibiting the central role of PLA2 in the
CC   inflammatory component of Alzheimer's disease. The amino acid (I) allows
CC   sensitive and rapid screening and identification of inhibitors of
CC   phospholipase A2. This sequence represents the human PLA2 protein (also
CC   known as phosphatide 2-acyl hydrolase)
XX
SQ   Sequence 913 AA;

  Query Match           85.5%;  Score 2767.5;  DB 3;  Length 913;
  Best Local Similarity  87.6%;  Pred. No. 3.2e-248;
  Matches  537;  Conservative    5;  Mismatches   22;  Indels   49;  Gaps    6;

Qy         24 TGLLVLFCPAPCPFFFFEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYR 83
              ||    ||| |     :| | ||:           ||  |    :    :|||   |
Db        319 TGTFRFHCPA-C-----WEQE-LSI----------RLQDAPEEQLKAPLSALPSGQVVR 360

Qy         84 --------------------LRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 123
                                  ||||||||||||||||||||||||||||||||||||||||
Db        361 LVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 420

Qy        124 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 480

Qy        184 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA 540

Qy        244 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 600

Qy        304 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 660

Qy        364 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 720

Qy        424 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 780

Qy        484 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF---------- 533
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHFPLVSDSFREY 840
```

```
Qy        534 -SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 592
              : ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 SAPGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 900

Qy        593 RQAVQRRRQRRPH 605
              |||||||||||||
Db        901 RQAVQRRRQRRPH 913
```

RESULT 7
AAB74635
ID AAB74635 standard; protein; 913 AA.
XX
AC AAB74635;
XX
DT 21-MAY-2001 (first entry)
XX
DE Phospholipase A2 (PLA2) protein sequence SEQ ID NO:3.
XX
KW Phospholipase A2; PLA2; antiinflammatory; inflammatory condition;
KW rheumatoid arthritis; psoriasis; asthma; cytosolic PLA2; cPLA2.
XX
OS Homo sapiens.
XX
PN US6197569-B1.
XX
PD 06-MAR-2001.
XX
PF 07-FEB-2000; 2000US-00500358.
XX
PR 29-MAR-1996; 96US-0014608P.
PR 19-MAR-1997; 97US-0041264P.
PR 28-MAR-1997; 97US-00827208.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Choiu XC, Kramer RM, Pickard RT, Sharp JD, Strifler BA;
XX
DR WPI; 2001-256372/26.
DR N-PSDB; AAF74998, AAF74999.
XX
PT Novel nucleic acid molecules encoding phospholipase A2 enzyme, useful in
PT screening assays for identifying compounds that inhibit or block
PT phospholipase A2 enzyme activity.
XX
PS Claim 1; Col 53-58; 32pp; English.
XX
CC The present invention describes an isolated polynucleotide (I),
CC comprising a 3085 base pair phospholipase A2 (PLA2) sequence (given in
CC AAF74999), encoding a 913 residue phospholipase A2 protein sequence
CC (given in AAB74635), or a nucleotide sequence which hybridises under
CC stringent conditions to the above mentioned nucleotide sequence. Also
CC described are: (1) an isolated polynucleotide (II) comprising an 8517
CC base pair sequence, given in AAF74998; (2) an expression vector (III)
CC comprising (I) and an expression control sequence; (3) a host cell
CC transformed with (III); (4) an expression vector (IV) comprising (II)
CC operably linked to an expression control sequence; and (5) a host cell
CC transformed with (IV). (I) is useful for screening compounds which
CC inhibit or block cytosolic PLA2 (cPLA2) enzyme activity. The host cells
CC transformed or transformed or transfected with cPLA2 enzymes in large
CC quantities which are useful in screening assays for discovering agents
CC that inhibit PLA2. The inhibitors identified are useful for treating
CC inflammatory conditions such as rheumatoid arthritis, psoriasis, or
CC asthma. (I) is also useful in the detection of mutant genomic DNA which
CC has been digested with restriction enzymes and run on an electrophoretic
CC gel by hybridising to the genomic DNA
XX
SQ Sequence 913 AA;

Query Match 85.5%; Score 2767.5; DB 4; Length 913;
Best Local Similarity 87.6%; Pred. No. 3.2e-248;
Matches 537; Conservative 5; Mismatches 22; Indels 49; Gaps 6;

```
Qy         24 TGLLVLFCPAPCPFFFFFEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYR 83
              ||      ||| |     :| | ||:           || |   :   :|||     |
Db        319 TGTFRFHCPA-C-----WEQE-LSI----------RLQDAPEEQLKAPLSALPSGQVVR 360

Qy         84 -------------------LRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 123
                                 ||||||||||||||||||||||||||||||||||||||||
Db        361 LVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 420

Qy        124 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 480

Qy        184 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA 540

Qy        244 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 600

Qy        304 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 660

Qy        364 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 720

Qy        424 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 780

Qy        484 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF---------- 533
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHFPLVSDAFREY 840

Qy        534 -SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 592
              : ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 SAPGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 900

Qy        593 RQAVQRRRQRRPH 605
              |||||||||||||
Db        901 RQAVQRRRQRRPH 913
```

RESULT 8
AAB82415
ID AAB82415 standard; protein; 913 AA.
XX
AC AAB82415;
XX
DT 06-AUG-2001 (first entry)
XX
DE Human phospholipase A2.
XX
KW Phospholipase A2; PLA2; bPLA2; PLA2-beta; inhibitor; screening;
KW antiinflammatory; human; Alzheimer's disease; therapy.
XX
OS Homo sapiens.
XX
PN US6242206-B1.
XX
PD 05-JUN-2001.
XX
PF 07-FEB-2000; 2000US-00498809.
XX
PR 29-MAR-1996; 96US-0014608P.
PR 19-MAR-1997; 97US-0041264P.
PR 28-MAR-1997; 97US-00827208.
XX
PA (ELIL) LILLY & CO ELI.
XX

REFERENCE IV

```
FT                   /organism='Mus musculus (mouse)'.
FEATURES             Location/Qualifiers
     source          1. .501
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
ORIGIN

  Query Match           45.4%;  Score 268.8;  DB 6;  Length 501;
  Best Local Similarity  77.7%;  Pred. No. 2.2e-57;
  Matches  324;  Conservative    0;  Mismatches   93;  Indels    0;  Gaps    0;

Qy         65 GCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACCAAGATGGTCAAGCAAGTG 124
Db          1 GCGGNTATAACTGCAACCCAGGGAGGGCTCCTGAACCTGAACAAGATGGTCACACACATG 60

Qy        125 ACTGGGAAAATGCCCATCTTCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGC 184
Db         61 ACGGGGAAGAAAGCCTTCTTCAGCTACTGGCCCTACGGCTGTCACTGTGGACTTGGTGGC 120

Qy        185 AGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGAC 244
Db        121 AAAGGGCAACCCAAAGATGCCACAGACTGGTGCTGTCAGAAGCATGATTGTTGCTATGCC 180

Qy        245 CACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTTTTCCCAG 304
Db        181 CACCTGAAGATCGATGGATGCAAGAGCCTGACAGACAACTACAAATACAGCATCTCCCAG 240

Qy        305 GGGAACATCCACTGCTCTGACAAGGGAAGCTGGTGTGAGCAGCAGCTGTGTGCCTGTGAC 364
Db        241 GGCACTATCCAGTGCTCTGACAACGGGAGCTGGTGTGAAAGGCAACTGTGTGCTTGTGAC 300

Qy        365 AAGGAGGTGGCCTTCTGCCTGAAGCGCAACCTGGACACCTACCAGAAGCGACTGCGTTTC 424
Db        301 AAGGAGGTGGCCTTGTGCTTGAAGCAAAACCTGGATAGCTACAATAAGCGCCTGCGTTAC 360

Qy        425 TACTGGCGGCCCCACTGCCGGGGGCAGACCCCTGGGTGCTAGAAGCCCACACCCTCT 481
Db        361 TACTGGCGGCCCCCGTTGCAAAGGCAAGACTCCAGCATGCTAAGGCAGTCCACTCTGT 417
```

RESULT 14
CPIIPHA2

```
LOCUS       CPIIPHA2                  760 bp    mRNA    linear   ROD 25-FEB-2003
DEFINITION  C.porcellus mRNA for typeII phospholipase A2.
ACCESSION   X82631
VERSION     X82631.1  GI:951010
KEYWORDS    phospholipase a2.
SOURCE      Cavia porcellus (domestic guinea pig)
  ORGANISM  Cavia porcellus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
REFERENCE   1
  AUTHORS   Vial,D., Senorale-Pose,M., Havet,N., Molio,L., Vargaftig,B.B. and
            Touqui,L.
  TITLE     Expression of the type-II phospholipase A2 in alveolar macrophages.
            Down-regulation by an inflammatory signal
  JOURNAL   J. Biol. Chem. 270 (29), 17327-17332 (1995)
  MEDLINE   95340522
   PUBMED   7615534
REFERENCE   2  (bases 1 to 760)
  AUTHORS   Vial,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-NOV-1994) D. Vial, Institut Pasteur, 25 rue du Dr.
            Roux, 75015 Paris, FRANCE
FEATURES             Location/Qualifiers
     source          1. .760
                     /organism="Cavia porcellus"
                     /mol_type="mRNA"
                     /strain="Hartley"
                     /db_xref="taxon:10141"
                     /cell_type="alveolar macrophage"
                     /dev_stage="adult"
     CDS             54. .491
                     /EC_number="3.1.1.4"
                     /codon_start=1
                     /product="typeII phospholipase A2"
                     /protein_id="CAA57953.1"
                     /db_xref="GI:951011"
                     /db_xref="GOA:P47711"
                     /db_xref="SWISS-PROT:P47711"
                     /translation="MKLLLLLLVVMASDLPQAHGHLKQFTEMIKLTTGKNGLTSYGAY
                     GCHCGVGGKGTPKDATDRCCVRHDCCYDRLMKRGCGTKFLNYRFTHKGSSITCSVKQN
                     SCQKQLCECDKAAAYCFAANLKSYSRRYQFYYNGLCRGKTPSC"
     sig_peptide     54. .113
     mat_peptide     114. .488
                     /product="unnamed"
     polyA_signal    552. .557
     polyA_signal    744. .749
ORIGIN

  Query Match           22.6%;  Score 133.8;  DB 10;  Length 760;
  Best Local Similarity  55.5%;  Pred. No. 3.7e-23;
  Matches  258;  Conservative    0;  Mismatches  207;  Indels    0;  Gaps    0;

Qy         26 ATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGTGATGGCTGGTGTGATTCCAATCCAG 85
Db         51 AGCATGAAGCTCCTCCTGCTGCTTCTGGTGGTCATGGCCTCTGACTTGCCTCAAGCCCAC 110

Qy         86 GGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGACTGGGAAAATGCCCATCCTC 145
Db        111 GGACACTTGAAGCAATTCACAGAAATGATCAAGCTCACGACAGGAAAGAATGGACTTACA 170

Qy        146 TCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAGAGGCCAACCCAAAGATGCC 205
Db        171 AGTTATGGCGCCTATGGCTGTCACTGTGGTGTGGGTGGCAAAGGAACTCCCAAGGATGCA 230

Qy        206 ACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCACCTGAAGACCCAGGGGTGC 265
Db        231 ACAGATAGGTGCTGTGTCAGGCATGACTGTTGCTATGACCGTCTGATGAAGCGTGGATGT 290

Qy        266 GGCATCTACAAGGACTATTACAGATACAACTTTTCCCAGGGGAACATCCACTGCTCTGAC 325
Db        291 GGCACGAAATTTCTGAACTACCGGTTTACCCATAAGGGGAGCTCGATCACCTGCAGTGTA 350

Qy        326 AAGGGAAGCTGGTGTGAGCAGCAGCTGTGTGCCTGTGACAAGGAGGTGGCCTTCTGCCTG 385
Db        351 AAGCAGAACTCCTGTCAGAAGCAGCTGTGTGAATGTGATAAAGCTGCTGCCTACTGTTTT 410

Qy        386 AAGCGCAACCTGGACACCTACCAGAAGCGACTGCGTTTCTACTGGCGGCCCCACTGCCGG 445
Db        411 GCTGCAAACCTGAAAAGTTATAGCAGAAGGTACCAGTTTTATTACAATGGACTGTGCCGC 470

Qy        446 GGGCAGACCCCTGGGTGCTAGAAGCCCACACCCTCTACCCTGTTC 490
Db        471 GGGAAGACCCCGAGTTGCTGAGAGCCACCGTGCTGAATCTTCTTC 515
```

RESULT 15
AR274880

```
LOCUS       AR274880                  1016 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 17 from patent US 6506607.
ACCESSION   AR274880
VERSION     AR274880.1  GI:29707430
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1016)
  AUTHORS   Shyjan,A.W.
  TITLE     Methods and compositio                    tification and assessment of
            prostate cancer therap                    gnosis of prostate cancer
  JOURNAL   Patent: US 6506607-A 1
FEATURES             Location/Qual
     source          1. .1016
                     /organism="unl
```